



SEQUENCE LISTING

#14

<110> Lanes, Olav
Willasen, Nils Peder
Guddal, Per Henrik
Gjellesvik, Dag Rune

<120> Cod uracil-DNA glycosylase, gene coding therefore,
recombinant DNA containing said gene or operative parts
thereof, a method for preparing said protein and the
use of said protein or said operative pa

<130> U013209-3

<140> 09/758,017

<141> 2001-01-10

<150> 2000 5428

<151> 2000-10-27

<150> 2000 0163

<151> 2000-01-12

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 1283

<212> DNA

<213> Gadus morhua

<220>

<221> CDS

<222> (18)..(920)

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ata tca tca aat cgg gty tta cca ggt tta cta att ccc caa act tta 98

Ile Ser Ser Asn Arg Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu

15

20

25

tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca 146

Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser

30

35

40

aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg gag cag ctg	194
Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu	
45 50 55	
gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag att aga gca	242
Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala	
60 65 70 75	
aaa gca acg cct gca ggt ttc gga gag act tgg aga aga gag ctg gct	290
Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala	
80 85 90	
gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc ttt gta gct	338
Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala	
95 100 105	
gat gag agg agc cgt cac acc gtc tac cca ccg gct gat caa gtg tac	386
Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr	
110 115 120	
agt tcg aca gag atg tgt gac att caa gat gtg aaa gta gtg att cta	434
Ser Ser Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu	
125 130 135	
ggc cag gac cct tac cac ggt ccc aac caa gca cat gga ctc tgt ttc	482
Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe	
140 145 150 155	
agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg aac ata tac	530
Ser Val Gln Lys Pro Val Pro Pro Pro Ser Leu Val Asn Ile Tyr	
160 165 170	
aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct gga cat gga	578
Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro Gly His Gly	
175 180 185	
gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt aac gcg gtg	626
Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val	
190 195 200	
ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac aga ggc tgg	674
Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp Arg Gly Trp	
205 210 215	
gag acc ttc acc gac gct gtg atc aag tgg ctg agc gtc aac cgg gaa	722
Glu Thr Phe Thr Asp Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu	
220 225 230 235	

gga gtc gtt ttc ctg ttg tgg ggc tca tac gcc cat aag aag gga gcg 770
 Gly Val Val Phe Leu Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala
 240 245 250

acc atc gac agg aaa cgt cac cat gtc ttg caa gct gtt cat cca tct 818
 Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Val His Pro Ser
 255 260 265

cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac ttc tcc aag 866
 Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys
 270 275 280

gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata aac tgg aga 914
 Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg
 285 290 295

gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga tgaacatcac 970
 Ala Leu
 300

actatatattt ctacagcttt tccaagttca aaccaatcta taagctttca tttgtctttt 1030

ggaatgatgc tgcttttggg cggttttaga tacttaaaac actttaccac tctgccatgt 1090

tgactcatgt tcagtcaata taactttcac aacttgaaca aaaatgttat ttataattg 1150

attatatattt gtacattaaa gattgttttt ttcccagggt gtttcatagg tactaggata 1210

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<211> 301

<212> PRT

<213> Gadus morhua

<400> 2

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Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
 35 40 45

Thr	Ser	Ser	Pro	Gln	Leu	Ser	Val	Glu	Gln	Leu	Glu	Arg	Met	Ala	Lys	50	55	60	
Asn	Lys	Lys	Ala	Ala	Leu	Asp	Lys	Ile	Arg	Ala	Lys	Ala	Thr	Pro	Ala	65	70	75	80
Gly	Phe	Gly	Glu	Thr	Trp	Arg	Arg	Glu	Leu	Ala	Ala	Glu	Phe	Glu	Lys	85	90	95	
Pro	Tyr	Phe	Lys	Gln	Leu	Met	Ser	Phe	Val	Ala	Asp	Glu	Arg	Ser	Arg	100	105	110	
His	Thr	Val	Tyr	Pro	Pro	Ala	Asp	Gln	Val	Tyr	Ser	Ser	Thr	Glu	Met	115	120	125	
Cys	Asp	Ile	Gln	Asp	Val	Lys	Val	Val	Ile	Leu	Gly	Gln	Asp	Pro	Tyr	130	135	140	
His	Gly	Pro	Asn	Gln	Ala	His	Gly	Leu	Cys	Phe	Ser	Val	Gln	Lys	Pro	145	150	155	160
Val	Pro	Pro	Pro	Pro	Ser	Leu	Val	Asn	Ile	Tyr	Lys	Glu	Leu	Cys	Thr	165	170	175	
Asp	Ile	Asp	Gly	Phe	Lys	His	Pro	Gly	His	Gly	Asp	Leu	Ser	Gly	Trp	180	185	190	
Ala	Lys	Gln	Gly	Val	Leu	Leu	Leu	Asn	Ala	Val	Leu	Thr	Val	Arg	Ala	195	200	205	
His	Gln	Ala	Asn	Ser	His	Lys	Asp	Arg	Gly	Trp	Glu	Thr	Phe	Thr	Asp	210	215	220	
Ala	Val	Ile	Lys	Trp	Leu	Ser	Val	Asn	Arg	Glu	Gly	Val	Val	Phe	Leu	225	230	235	240
Leu	Trp	Gly	Ser	Tyr	Ala	His	Lys	Lys	Gly	Ala	Thr	Ile	Asp	Arg	Lys	245	250	255	
Arg	His	His	Val	Leu	Gln	Ala	Val	His	Pro	Ser	Pro	Leu	Ser	Ala	His	260	265	270	
Arg	Gly	Phe	Leu	Gly	Cys	Lys	His	Phe	Ser	Lys	Ala	Asn	Gly	Leu	Leu	275	280	285	
Lys	Leu	Ser	Gly	Thr	Glu	Pro	Ile	Asn	Trp	Arg	Ala	Leu	290	295	300				

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Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly
10 15 20

agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257
Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val
45 50 55

att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353
Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg
75 80 85

ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449
Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp
105 110 115 120

5

125	130	135	
gtg att cta ggc cag gac cct tac cac ggt ccc aac caa gca cat gga			545
Val Ile Leu Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly			
140	145	150	
ctc tgt ttc agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg			593
Leu Cys Phe Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val			
155	160	165	
aac ata tac aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct			641
Asn Ile Tyr Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro			
170	175	180	
gga cat gga gat cta agc gga tgg gca aac aag ggg tgc tgc tgc tta			689
Gly His Gly Asp Leu Ser Gly Trp Ala Asn Lys Gly Cys Cys Cys Leu			
185	190	195	200
acg cgc tgc ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac			737
Thr Arg Cys Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp			
205	210	215	
aga ggc tgg gag acc tcc acc gac gct gtg atc aag tgg ctg agc gtc			785
Arg Gly Trp Glu Thr Ser Thr Asp Ala Val Ile Lys Trp Leu Ser Val			
220	225	230	
aac cgg gaa gga gtg gtt ttc ctg ttc tgg ggc tca tac gcc cat aag			833
Asn Arg Glu Gly Val Val Phe Leu Phe Trp Gly Ser Tyr Ala His Lys			
235	240	245	
aag gga gcg acc atc gac agg aaa cgt cac cat gtc ttg caa gct ctt			881
Lys Gly Ala Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Leu			
250	255	260	
cat cca tct cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac			929
His Pro Ser Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His			
265	270	275	280
ttc tcc aag gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata			977
Phe Ser Lys Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile			
285	290	295	
aac tgg aga gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga			1032
Asn Trp Arg Ala Leu			
300			
tgaacatcac actatatttt ctacagcttt tccaagttca aaccaatcta taagctttca			1092

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<210> 4
 <211> 301
 <212> PRT
 <213> Gadus morhua

<400> 4
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 Val Gln Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
 35 40 45
 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
 50 55 60
 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
 65 70 75 80
 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
 85 90 95

Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
 100 105 110
 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
 115 120 125
 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
 130 135 140
 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
 145 150 155 160
 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr

	165		170		175
Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp					
	180		185		190
Ala Asn Lys Gly Cys Cys Cys Leu Thr Arg Cys Leu Thr Val Arg Ala					
	195		200		205
His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Ser Thr Asp					
	210		215		220
Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu					
	225		230		235
Phe Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys					
		245		250	255
Arg His His Val Leu Gln Ala Leu His Pro Ser Pro Leu Ser Ala His					
	260		265		270
Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu					
	275		280		285
Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu					
	290		295		300

<210> 5
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial
 Sequence - Primer used to generate cDNA of a
 fragment of UNG gene

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<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial

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fragment of UNG gene

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<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
Sequence - Primer used to generate cDNA portion
of cUNG gene

<400> 7
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<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
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<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
Sequence - Primer used to generate fragment of UNG
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<400> 9
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<220>
 <223> Description of Artificial Sequence: Artificial
 Sequence - Primer used to construct rcUNG delta 74
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<210> 14
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 <212> DNA
 <213> Artificial Sequence

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<400> 14
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<210> 15
 <211> 33
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Artificial
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<210> 16
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 <212> DNA
 <213> Artificial Sequence

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 Sequence - Primer used to construct rcUNG delta
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<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

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<210> 18

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
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<210> 19

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence - Primer used to prepare rcUNG gene

<400> 19

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